

# SEQUENCE LISTING

<110> WANG, XIAODONG  
LIU, XUESONG

<120> DNA FRAGMENTATION FACTOR INVOLVED IN APOPTOSIS

<130> UTSD:546USD1

<140> UNKNOWN

<141> 2000-12-22

<150> 09/061,702

<151> 1998-04-16

<160> 21

<170> PatentIn Ver. 2.1

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<212> DNA

<213> Homo sapiens

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<213> Homo sapiens

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35 40 45

Tyr Glu Asp Gly Thr Glu Leu Thr Glu Asp Tyr Phe Pro Ser Val Pro  
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Asp Asn Ala Glu Leu Val Leu Leu Thr Leu Gly Gln Ala Trp Gln Gly  
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002227-132200

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Val	Gly	Leu	Ile	Gln	Ala	Ala	Gln	Gln	Leu	Leu	Cys	Asp	Glu	Gln	Ala	100	105	110	
Pro	Gln	Arg	Gln	Arg	Leu	Leu	Ala	Asp	Leu	Leu	His	Asn	Val	Ser	Gln	115	120	125	
Asn	Ile	Ala	Ala	Glu	Thr	Arg	Ala	Glu	Asp	Pro	Pro	Trp	Phe	Glu	Gly	130	135	140	
Leu	Glu	Ser	Arg	Phe	Gln	Ser	Lys	Ser	Gly	Tyr	Leu	Arg	Tyr	Ser	Cys	145	150	155	160
Glu	Ser	Arg	Ile	Arg	Ser	Tyr	Leu	Arg	Glu	Val	Ser	Ser	Tyr	Pro	Ser	165	170	175	
Thr	Val	Gly	Ala	Glu	Ala	Gln	Glu	Glu	Phe	Leu	Arg	Val	Leu	Gly	Ser	180	185	190	
Met	Cys	Gln	Arg	Leu	Arg	Ser	Met	Gln	Tyr	Asn	Gly	Ser	Tyr	Phe	Asp	195	200	205	
Arg	Gly	Ala	Lys	Gly	Gly	Ser	Arg	Leu	Cys	Thr	Pro	Glu	Gly	Trp	Phe	210	215	220	
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Val	Glu	Ala	Ile	Lys	Glu	Gln	Asp	Gly	Arg	Glu	Val	Asp	Trp	Glu	Tyr	275	280	285	
Phe	Tyr	Gly	Leu	Leu	Phe	Thr	Ser	Glu	Asn	Leu	Lys	Leu	Val	His	Ile	290	295	300	
Val	Cys	His	Lys	Lys	Thr	Thr	His	Lys	Leu	Asn	Cys	Asp	Pro	Ser	Arg	305	310	315	320
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Met Glu

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gtg acc ggg gac gcc ggg gta cca gaa tct ggc gag atc cgg act cta 166  
Val Thr Gly Asp Ala Gly Val Pro Glu Ser Gly Glu Ile Arg Thr Leu  
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Lys Pro Cys Leu Leu Arg Arg Asn Tyr Ser Arg Glu Gln His Gly Val  
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Ala Ala Ser Cys Leu Glu Asp Leu Arg Ser Lys Ala Cys Asp Ile Leu  
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gcc att gat aag tcc ctg aca cca gtc acc ctt gtc ctg gca gag gat 310  
Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala Glu Asp  
55 60 65

ggc acc ata gtg gat gat gac gat tac ttt ctg tgt cta cct tcc aat 358  
Gly Thr Ile Val Asp Asp Asp Asp Tyr Phe Leu Cys Leu Pro Ser Asn  
70 75 80

act aag ttt gtg gca ttg gct agt aat gag aaa tgg gca tac aac aat 406  
Thr Lys Phe Val Ala Leu Ala Ser Asn Glu Lys Trp Ala Tyr Asn Asn  
85 90 95

tca gat gga ggt aca gct tgg att tcc caa gag tcc ttt gat gta gat 454  
Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp Val Asp  
100 105 110

002221" T5484250

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Leu Lys Glu Asp	135				Ser Ser Ile Ile	140				Leu Leu Ser Glu Glu Asp	145			Leu		
cag atg ctt gtt gac gct ccc tgc tca gac ctg gct cag gaa cta cgt																598
Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu Leu Arg	150				155				160							
cag agt tgt gcc acc gtc cag cgg ctg cag cac aca ctc caa cag gtg																646
Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln Gln Val	165				170				175							
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Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu Gln Leu	180				185				190							
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Tyr Leu Gln Ala Leu Glu Lys Glu Gly Ser Leu Leu Ser Lys Gln Glu	200				205				210							
gag tcc aaa gct gcc ttt ggt gag gag gtg gat gca gta gac acg ggt																790
Glu Ser Lys Ala Ala Phe Gly Glu Glu Val Asp Ala Val Asp Thr Gly	215				220				225							
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Met Ser Arg Glu Thr Ser Ser Asp Val Ala Leu Ala Ser His Ile Leu	230				235				240							
act gca ctg agg gag aag cag gct cca gag ctg agc tta tct agt cag																886
Thr Ala Leu Arg Glu Lys Gln Ala Pro Glu Leu Ser Leu Ser Ser Gln	245				250				255							
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Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala Val Ala	260				265				270							
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Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala Cys Glu	275				280				285				290			
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Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His Ser Leu	295				300				305							

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 Pro Lys Arg Ala Arg Gln Asp Pro Thr  
 325 330

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Ile Leu Ala Ile Asp Lys Ser Leu Thr Pro Val Thr Leu Val Leu Ala  
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Glu Asp Gly Thr Ile Val Asp Asp Asp Asp Tyr Phe Leu Cys Leu Pro

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Asn Asn Ser Asp Gly Gly Thr Ala Trp Ile Ser Gln Glu Ser Phe Asp						
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Val Asp Glu Thr Asp Ser Gly Ala Gly Leu Lys Trp Lys Asn Val Ala						
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Arg Glu Leu Lys Glu Asp Leu Ser Ser Ile Ile Leu Leu Ser Glu Glu						
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Asp Leu Gln Met Leu Val Asp Ala Pro Cys Ser Asp Leu Ala Gln Glu						
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Leu Arg Gln Ser Cys Ala Thr Val Gln Arg Leu Gln His Thr Leu Gln						
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Gln Val Leu Asp Gln Arg Glu Glu Val Arg Gln Ser Lys Gln Leu Leu						
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Ser Gln Asp Leu Glu Leu Val Thr Lys Glu Asp Pro Lys Ala Leu Ala						
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Val Ala Leu Asn Trp Asp Ile Lys Lys Thr Glu Thr Val Gln Glu Ala						
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Cys Glu Arg Glu Leu Ala Leu Arg Leu Gln Gln Thr Gln Ser Leu His						
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00222T "TSH3H260

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 117. *Chlorophyll akz* (Chl *akz*)  
 118. *Chlorophyll alz* (Chl *alz*)  
 119. *Chlorophyll amz* (Chl *amz*)  
 120. *Chlorophyll anz* (Chl *anz*)  
 121. *Chlorophyll aoz* (Chl *aoz*)  
 122. *Chlorophyll apz* (Chl *apz*)  
 123. *Chlorophyll aqz* (Chl *aqz*)  
 124. *Chlorophyll arz* (Chl *arz*)  
 125. *Chlorophyll asz* (Chl *asz*)  
 126. *Chlorophyll atz* (Chl *atz*)  
 127. *Chlorophyll auz* (Chl *auz*)  
 128. *Chlorophyll avz* (Chl *avz*)  
 129. *Chlorophyll awz* (Chl *awz*)  
 130. *Chlorophyll axz* (Chl *axz*)  
 131. *Chlorophyll ayz* (Chl *ayz*)  
 132. *Chlorophyll ayz* (Chl *ayz*)  
 133.

<223> D = G, C or A

<223> Description of Artificial Sequence: Synthetic  
Primer

17

30

30

31

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<400> 21  
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1 5

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